


```

Db 465 LSTTIFQIVLSLVGVSSQIDNQPDLQ 492

RESULT 3
E88571
A:Title: G05B5-5 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: E88571
R:anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99065613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans
A:Accession: E88571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: GB:chr_III; PIDN:CA83593.1; PID:g3873993; GSPDB:GN00021; CESP:C05B5
C:Genetics:
A:Gene: C05B5.5
A:Map position: 3

Query March 29.0%; Score 60; DB 2; Length 585;
Best Local Similarity 46.4%; Pred. NO. 5.3;
Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 7 LTGWIVLVSVLLGVASHIDNYPPEQ 34
| | | | | | | | | | | | | | |
Db 465 LSTTIFQIVLSLVGVSSQIDNQPDLQ 492

RESULT 4
I64215
A:hypothetical protein MG144 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1995
C:Accession: I64215
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhman, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
A:Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: I64215
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-279 <TIGR>
A:Cross-references: GB:U39694; GB:L43967; NID:g1045822; PID:g1045827; TIGR:MG144
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3

Query Match 27.5%; Score 57; DB 2; Length 279;
Best Local Similarity 36.1%; Pred. NO. 6.5;
Matches 13; Conservative 8; Mismatches 7; Indels 8; Gaps 1;

QY 2 NRLELTGMIVLVSVLLGVA-----SHIDNY 29
| | | | | | | | | | | | | | |
Db 231 SRSTHFTWIVLTIVLVLLVSCLLMIAVAHHDGT 266

RESULT 5
A55542
A:sensor kinase rege - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: A55542
R:Moyley, C.S.; Suzuki, J.Y.; Bauer, C.E.
J. Bacteriol. 176, 7566-7573, 1994
A:Title: Identification and molecular genetic characterization of a sensor kinase respon

```

```

A:Reference number: A55542; MUID:95095926; PMID:8002581
A:Accession: A55542
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-441 <MOS>
A:Cross-references: gb-b55179
C:Genetics:
A:Gene: regB
C:Keywords: transmembrane protein

Query Match      27.5%; Score 57; DB 2; Length 441;
Best Local Similarity 40.9%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 4 LIELTGMIVLVSVILGVASH 25
Db 146 MIEFGSWAIVIGVIFLGAYAH 167
      || | : : | | | | : |
      || | : : | | | | : |

RESULT 6
T11105
H:-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - side-necked turtle mitoc
C:Species: mitochondrion Pelomedusa subrufa
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11105
R:Zardoya, R.; Meyer, A.
Proc. Natl. Acad. Sci. U.S.A. 95, 14226-14231, 1998
A:Title: Complete mitochondrial genome suggests diapsid affinities of turtles.
A:Reference number: 217248; MUID:99045666; PMID:9826682
A:Accession: T11105
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-55 <AR>
A:Cross-references: EMBL:AF039066; NID:g3599976; PID:g3599981; PIDN:AAD05054.1
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: H+-transporting ATP synthase protein 8
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match      26.8%; Score 55.5; DB 2; Length 55;
Best Local Similarity 37.0%; Pred. No. 2.1;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

OY 5 IELTGMIVLVSVILGVASHDNTOP 31
Db 12 IFITSMILIT-ILPKIKSHIPNNSP 37
      | : | | : : | : | | | |
      | : | | : : | : | | | |

RESULT 7
S62354
hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: T38593; S62354
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A:Reference number: 221801
A:Accession: T38593
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <PE2>
A:Cross-references: EMBL:Z67961; NID:g1065887; PIDN:CMA91892.1; PID:g1065893, GSPDB:
A:Experimental source: strain 972h-; cosmid c30D11
C:Genetics:
A:Gene: SPAC30D11.06c
A:Map position: 1L
A:Introns: 46/2; 75/3

Query Match      26.8%; Score 55.5; DB 2; Length 426;
Best Local Similarity 28.9%; Pred. No. 15;
Matches 11; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

OY 2 NRLIELTGMIVLVSVI-LLGVAASHDNTQPEQASV 38

```

Db	3 NEIYALCGFFVAIALVLCSTISTITHLKNKKPVLORSV 40	Genome Res. 11, 731-753, 2001 A:Title: The complete genome sequence of the lactic acid bacterium <i>Lactococcus lactis</i> A:Reference number: AB6625; MUID:21235186; PMID:11337471 A:Accession: F66821 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-320 <STO> A:Cross-references: GB:AE005176; PID:g12724578; PIDN:AAK05672.1; GSPDB:GN00146 C:Genetics: A:Gene: yqdb
RESULT 8	H95210	
type IV prepeilin peptidase, probable [imported] - Streptococcus pneumoniae (strain TIGR4		
C:Species: Streptococcus pneumoniae		
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001		
C:Accession: H95210		
R:Retelin, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held		
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,		
nson, T.; Hickey, E.K.; Holt, I.E.		
Science 293, 498-506, 2001		
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,		
A:Title: Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> .		
A:Reference number: A95000; MUID:21357209; PMID:11463916		
A:Accession: H95210		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-219 <KUR>		
A:Cross-references: GB:AE005672; PIDN:AAK75881.1; PID:g14973307; GSPDB:GN00164; TIGR:SP4		
C:Genetics:		
A:Experimental source: strain TIGR4		
A:Gene: SPI808		
Query Match	26.6%; Score 55; DB 2; Length 219;	
Best Local Similarity	40.9%; Pred. No. 9.4;	
Matches	9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;	
QY	4 LIETGWIYLVVSVIIIGVASH 25	
Db	127 LIASGWNLMVWSFIIIGIAH 148	
RESULT 9	B98075	
type 4 prepeilin peptidase (EC 3.4.-.-) [imported] - Streptococcus pneumoniae (strain R6)		
C:Species: Streptococcus pneumoniae		
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001		
C:Accession: B98075		
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; F		
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M		
y, P.; Sun, P.M.; Winkler, M.E.		
J. Bacteriol. 183, 5709-5717, 2001		
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balte, R.H.; Jaskunas, S.R.;		
A:Title: Genome of the Bacterium <i>Streptococcus pneumoniae</i> Strain R6.		
A:Reference number: A97872; MUID:21429245; PMID:11544234		
A:Accession: B98075		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-219 <KUR>		
A:Cross-references: GB:AE007317; PIDN:AAU00431.1; PID:g15459298; GSPDB:GN00174		
C:Genetics:		
A:Gene: PILD		
C:Keywords: hydrolase		
Query Match	26.6%; Score 55; DB 2; Length 219;	
Best Local Similarity	40.9%; Pred. No. 9.4;	
Matches	9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;	
QY	4 LIETGWIYLVVSVIIIGVASH 25	
Db	127 LIASGWNLMVWSFIIIGIAH 148	
RESULT 10	F66821	
hypothetical protein yqbf [imported] - <i>Lactococcus lactis</i> subsp. <i>lactis</i> (strain IL1403)		
C:Species: <i>Lactococcus lactis</i> subsp. <i>lactis</i>		
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001		
C:Accession: F66821		
R:Boitlin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Mairame, K.; Weissenbach, J.; Ehrli		

Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*
A:Reference number: AB6625; MUID:21235186; PMID:11337471
A:Accession: F66821
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <STO>
A:Cross-references: GB:AE005176; PID:g12724578; PIDN:AAK05672.1; GSPDB:GN00146
C:Genetics:
A:Gene: yqdb

Query Match 26.6%; Score 55; DB 2; Length 320;
Best Local Similarity 37.9%; Pred. No. 14;
Matches 11; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRLIETGWIYLVVSVIIIGVASHIDNY 29
Db 1 MKRRKMTAMILVLSVYVVGYPFAIMY 29

RESULT 11
F90361
transport membrane protein (permease) [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: F90361
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; (Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redde
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: F90361
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <KUR>
A:Cross-references: GB:AE006641; NID:g13815231; PIDN:AAK42149.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1958

Query Match 26.1%; Score 54; DB 2; Length 374;
Best Local Similarity 36.4%; Pred. No. 21;
Matches 16; Conservative 6; Mismatches 8; Indels 14; Gaps 2;

QY 4 LIETGWIYLVVSVI-----LLGVASHIDNTQPEOS 35
Db 266 LINTLGTILTFSTIFSNNDILPEAFILGIFSF--SYRPPPTS 307

RESULT 12
T42721
CRP-ductin-alpha precursor - mouse
C:Species: *Mus musculus* (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 23-Mar-2001
C:Accession: T42721
R:Cheng, H.; Bjerknes, M.; Chen, H.
Anat. Rec. 244, 327-343, 1996
A:Title: CRP-ductin: a gene expressed in intestinal crypts and in pancreatic and hep
A:Reference number: 422241; MUID:96362470; PMID:8742698
A:Accession: T42721
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7083 <CHS>

A:Cross-references: EMBL:U37438; NID:g1276646; PID:g1276647; PIDN:AAK52505.1
A:Experimental source: strain BALB/c; jejunal epithelial cells
C:Keywords: transmembrane protein
F:1-78/Domain: signal sequence #status predicted <SIG>
F:29-2083/Product: CRP-ductin-alpha #status predicted <MNT>

Query Match 26.1%; Score 54; DB 2; Length 2083;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:35:59 ; Search time 11 Seconds
(without alignments)
154.594 Million cell updates/sec

Title: US-09-828-456-2

Perfect score: 207

Sequence: 1 MNRLIELTGMIVLVSVILL.....VASHIDNXPPEOSASVOHK 41

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207	100.0	41	BLR_ECOLI	P56976 escherichia
2	207	100.0	60	YK05_CAERI	P39473 caenorhabdit
3	58.5	28.3	323	C108_MOUSE	Q94773 mus musculus
4	57	27.5	279	Y14_MYCGE	P47390 mycoplasma
5	55.5	26.8	55	ATP8_PELSU	O79674 pelomonada
6	55.5	26.8	426	YAH6_SCHPO	O09906 schizosacch
7	52.5	25.4	120	CHH1_PENUP	O15980 penaeus jap
8	52.5	25.4	120	CHH2_PENUP	O90562 penaeus jap
9	52.5	25.4	120	HEMA_PT3HV	P12364 human para
10	52.5	25.1	124	DHSC_RICCN	O92199 rickettsia
11	52	25.1	612	OCTC_BOVIN	O19094 bos taurus
12	51.5	24.9	307	O0X2_ACEAC	P50653 acetobacter
13	51	24.6	458	TCR_STRAG	P13924 streptococc
14	50.5	24.4	104	YH2_LACHE	P22295 lactobacilli
15	50.5	24.4	173	CCME_MAEIN	P45036 haemophilus
16	50.5	24.4	355	RHOW_DROME	P20350 drosophila
17	50	24.2	219	YDR6_SCHPO	O13748 schizosacch
18	50	24.2	226	ATP6_FELCA	P48894 felis silve
19	50	24.2	265	ASPX_HUMAN	P26436 homo sapien
20	50	24.2	1127	Y855_TREPA	O81827 treponema p
21	49.5	23.9	404	CYE_MARPO	P26852 marchantia
22	49.5	23.9	513	H0H1_STRPY	P58083 streptococc
23	49	23.7	226	ATP6_HIPAM	O94296 hippopotamu
24	49	23.7	431	PKR_RAT	O91787 rattus norv
25	49	23.7	545	ATPA_XENLA	P08428 xenopus lae
26	49	23.7	1462	T0P2_PEA	O24308 pisum sativ
27	48.5	23.4	323	C108_HUMAN	O94354 homo sapien
28	48.5	23.4	360	MRAY_PSEAE	O94354 pseudoanac
29	48	23.2	66	YPTB_TNVD	P27112 tobacco nec
30	48	23.2	124	DHSC_RICPR	P41085 rickettsia
31	48	23.2	263	RLPA_VIBCH	O9414 vibrio chol
32	48	23.2	402	KLFC_HUMAN	O9444 homo sapien
33	48	23.2	503	CIS_BACHD	O94824 bacillus ha

34	47.5	22.9	392	1	CYB_SOLTU	P29757 solanum tub
35	47.5	22.9	393	1	CYB_ARATH	P42792 arabidopsis
36	47.5	22.9	394	1	CYB_OENBE	P09843 oenothera b
37	47.5	22.9	422	1	EXUT_BACSU	O34456 bacillus su
38	47.5	22.9	1953	1	BIGA_SALTY	P25927 salmonella
39	47	22.7	224	1	UL01_HCMVA	P16719 human cytom
40	47	22.7	242	1	TRP2_CVACA	P34793 cyanidium c
41	47	22.7	461	1	FTSY_AQUAE	O67066 aquilex aeo
42	47	22.7	462	1	REGB_RHOSH	O53068 rhodobacter
43	47	22.7	612	1	OCTC_HUMAN	O9439 homo sapien
44	47	22.7	1603	1	VIT5_CAERI	P06125 caenorhabdi
45	46.5	22.5	203	1	BCRC_BACLI	P42334 bacillus li

ALIGNMENTS

RESULT 1	ID	BLR_ECOLI	STANDARD:	PRT:	41 AA.
AC	P56976:				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Beta-lactam resistance protein.				
GN	BLR OR B1624.1.				
OS	Escherichia coli.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OX	NCBI_TaxID=562;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-K12 / MG1655;				
RX	MEDLINE-9742617; PubMed-9278503;				
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Bernal N.T., Burland V.,				
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,				
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.D.,				
RA	Mau B., Zhao Y., McMurtry L.M., Levy S.B.;				
RT	Genes 217, 1-13 (1990).				
RL	Genes 217, 1-13 (1990).				
RM	IDENTIFICATION, AND CHARACTERIZATION.				
RP	STRAIN-K12;				
RC	MEDLINE-20392465; PubMed-10931331;				
RX	Wong R.S.Y., McMurtry L.M., Levy S.B.;				
RA	"intergenic" b1r gene in Escherichia coli encodes a 41-residue				
RT	membrane protein affecting intrinsic susceptibility to certain				
RI	inhibitors of peptidoglycan synthesis."				
RL	Mol. Microbiol. 7, 565-572 (1990).				
CC	-1- FUNCTION: HAS AN EFFECT ON THE SUSCEPTIBILITY TO A NUMBER OF				
CC	ANTIBIOTICS INVOLVED IN PEPTIDOGLYCAN BIOSYNTHESIS. ACTS WITH BETA				
CC	LACTAMS, D-CYCLOSERINE AND BACITRACIN. HAS NO EFFECT ON THE				
CC	SUSCEPTIBILITY TO TETRACYCLINE, CHLORAMPHENICOL, GENTAMICIN,				
CC	FOROXYCIN, VACOMYCIN OR QUINOLONES. MIGHT ENHANCE DRUG EXIT BY				
CC	BEING PART OF MULTISUBUNIT EFFLUX PUMP. MIGHT ALSO BE INVOLVED IN				
CC	CELL WALL BIOSYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: INNER MEMBRANE-BOUND.				
CC	-1- PTM: THE N-TERMINUS IS BLOCKED.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AE000258; -; NOT_ANNOTATED_CDS.				
DR	EMBL; AF219227; AAF82191.1; -.				
DR	Ecogene; EG14389; b1r.				
KW	Antibiotic resistance; Transmembrane; Inner membrane;				
KW	Complete proteome.				
FT	TRANSMEM 4 24 POTENTIAL.				

FT	DOMAIN	25	41	PERIPLASMIC (POTENTIAL).
SQ	SEQUENCE	41 AA; 4556 MM; D384EBB01276D46B CRC64;		
Query Match	Best Local Similarity	100.0%; Score 207; DB 1; Length 41;		
Matches	41; Conservative	0; Mismatches	0; Indels	0; Gaps
OY	1	MNRLEIETGIVLVSVYILGVASHIDNYQPPQSASVQHK	41	
Db	1	MNRLEIETGIVLVSVYILGVASHIDNYQPPQSASVQHK	41	
RESULT 2				
ID	YK05_CAEEL	STANDARD;	PRT;	585 AA.
AC	P34293;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	Hypothetical 66.5 kDa protein C0585.5 in chromosome III.			
GN	C0585.5.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelodermidae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN-Bristol N2;			
RA	Mortimore B.J.;			
RL	Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: Z32679; CAA83593.1; -			
DR	WormRep: C05B5.5; CE00051.			
DR	InterPro: IPR001810; F-box.			
DR	InterPro: IPR002899; WRI/EB.			
DR	Pfam: PF00646; F-box; 1.			
DR	Pfam: PF01683; EB; 2.			
DR	SMART: SM00256; FBOX; 1.			
DR	SMART: SM00289; WRI; 2.			
DR	PROSITE: PS50181; FBOX; 1.			
KW	Hypothetical protein.			
FT	DOMAIN	12	60	F-BOX.
SQ	SEQUENCE	585 AA; 66491 MM; E6951E9B854B8C69 CRC64;		
Query Match	Best Local Similarity	29.0%; Score 60; DB 1; Length 585;		
Matches	13; Conservative	7; Mismatches	8; Indels	0; Gaps
OY	7	LTGIVLVSVYILGVASHIDNYQPPQ	34	
Db	465	LSSTIFQIVSLVGVSSQIDDNQPEIQ	492	
RESULT 3				
ID	C108_MOUSE	STANDARD;	PRT;	323 AA.
AC	090Y73; Q9DIP9; Q991Y8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Protein C10f8 homolog precursor (Thymic dendritic cell-derived factor			
DE	1).			
GN	C10f8 OR TDCFL			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN-Bates; TISSUE-thymus,			
RA	Jin C.G., Chen W.F.;			
RT	"Isolation and molecular cloning of gene encoding a novel dendritic			
RL	cell-derived factor.";			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: AF116911; AAF20283.1; -			
DR	EMBL: AK003252; BAB22668.1; ALT_INIT.			
DR	EMBL: BC002164; AAH02164.1; -			
DR	MGI: 1929278; Tdcfl.			
FT	SIGNAL; Transmembrane.			
FT	CHAIN	1	34	POTENTIAL.
FT	CHAIN	35	323	POTENTIAL.
FT	TRANSMEM	240	262	POTENTIAL.
FT	CARBOHYD	90	90	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CONFLICT	48	48	C -> V (IN REF. 1).
FT	CONFLICT	103	103	A -> T (IN REF. 1).
FT	CONFLICT	121	121	L -> W (IN REF. 1).
FT	CONFLICT	139	139	H -> Q (IN REF. 1).
FT	CONFLICT	221	222	YL -> DR (IN REF. 1).
FT	CONFLICT	264	264	A -> G (IN REF. 1).
FT	CONFLICT	277	300	YGDLEPMNDKSRVAPSLVVR -> IGHFQFINQNLTF
FT	CONFLICT			TYPPPLITV (IN REF. 1).
SQ	SEQUENCE	323 AA; 36313 MM; 0E9BF6B6E07C7D96 CRC64;		
Query Match	Best Local Similarity	28.3%; Score 58.5; DB 1; Length 323;		
Matches	14; Conservative	9; Mismatches	4; Indels	9; Gaps

OY 8 TGMIV---LVSVILL-----GVASHINDYOPPO 34
 DB 238 SGMIITLTTLVSLVMTLMTICAAVATAVQVYPERK 273

RESULT 4

Y144_MYCGE STANDARD: PRT: 279 AA.
 AC P47390;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG144.
 GN MG144.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxId=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RC MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
 RA Tombl J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lueker T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 64-140 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RC MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;
 RT "A survey of the Mycoplasma genitalium genome by using random
 RT sequencing.";
 RL J. Bacteriol. 175:7918-7930(1993).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U02121; AAC12395.1; -;
 DR EMBL: U02121; AAC12395.1; -;
 DR TIGR: MG144; -;
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 156 176 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 237 257 POTENTIAL.
 SO SEQUENCE 279 AA: 31717 MW: 883842C99C2CC41 CRC64;

Query Match 27.5%; Score 57; DB 1; Length 279;
 Best Local Similarity 36.1%; Pred. No. 4.4;
 Matches 13; Conservative 8; Mismatches 7; Indels 8; Gaps 1;

OY 2 NRILELTGWIVVSVILGVA-----SHINDY 29
 DB 231 SRSHYFIWIVILINVLLVCLLMIAVAYHIDGY 266

RESULT 5
 ATP8_PELSU STANDARD: PRT: 55 AA.
 AC O79674;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).

GN MTAAP8 OR ATP8.
 OS Pelomedusa subrufa (African side-necked turtle).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
 OX NCBI_TaxId=44522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zardoya R.;
 RL Submitted (DRC-1997) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONCYTIC COMPONENT
 CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
 CC H(+) (out).
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
 CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF039066; AAC05054.1; -;
 DR InterPro: IPR001421; ATPase8_mlt.
 DR Pfam: PF00895; ATP-synt_8; 1.
 KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT TRANSMEM 4 24 POTENTIAL.
 SO SEQUENCE 55 AA: 6536 MW: D8D4BC8F8651A001 CRC64;

Query Match 26.8%; Score 55.5; DB 1; Length 55;
 Best Local Similarity 37.0%; Pred. No. 1.4;
 Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

OY 5 IELTGWIVVSVILGVASHINDYOP 31
 DB 12 IFITSMILITLILPKIKSHIPNNSP 37

RESULT 6
 YAU6_SCHPO STANDARD: PRT: 426 AA.
 AC Q009906;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C30D11.06c in chromosome I.
 GN SPAC30D11.06c.
 OS Schizosaccharomyces pombe (Fission Yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 OX NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RC MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidergoy J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritze C., Holzer E., Moschl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambitt R., Pirnalle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Inoue M., Roche M., Gattard C., Taitava V.R., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schistosoma japonicum* pombe.",
 RL Nature 415:671-680(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE DUF0206 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z67961; CAA91892.1; -;
 DR InterPro: IPR005178; DUF300.
 DR Pfam: PF03619; DUF300; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 73 93 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 223 243 POTENTIAL.
 SQ SEQUENCE 426 AA; 49289 MW; 963450D799C3078 CRC64;
 Query Match 26.8%; Score 55.5; DB 1; Length 426;
 Best Local Similarity 28.9%; Pred. No. 10;
 Matches 11; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
 QY 2 NRLELNGWLVVSVTLGVASHIDNYQPEQASV 38
 DB 3 NEIVALCGFVALVLCISITHLNKKRPVLRV 40
 RESULT 7
 CHH2_PENUP STANDARD; PRT; 120 AA.
 AC 015980;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Crustacean hyperglycemic hormone 1 precursor (CHH) (Pej-SGP-I).
 OS Penaeus japonicus (Kuruma prawn).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata;
 OC Penaeoidea; Penaeidae; Marsupenaeus.
 OX NCBI_Taxid=27405;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Eyestalk;
 RA Ohira T., Watanabe T., Nagasawa H., Aida K.;
 RT "Molecular cloning of cDNAs encoding four crustacean hyperglycemic
 RT hormones and a molt-inhibiting hormone from the kuruma prawn *Penaeus*
 RT *japonicus*.";
 RL (in) Proceedings of the XIII International congress of comparative
 RL endocrinology, pp.83-86, Yokohama (1998).
 RP [2]
 RP SEQUENCE OF 47-118.
 RC TISSUE-Sinus gland;
 RX MEDLINE=97353924; Pubmed=9210164;
 RA Yang W.-J., Aida K., Nagasawa H.;
 RT "Amino acid sequences and activities of multiple hyperglycemic
 RT hormones from the kuruma prawn, *Penaeus japonicus*.";
 RP Peptides 18:479-485(1997).

RN [3]
 RP SEQUENCE OF 47-101.
 RC TISSUE-Sinus gland;
 RA Yang W.-J., Aida K., Nagasawa H.;
 RT "Amino acid sequences of a hyperglycemic hormone and its related
 RT peptides from the kuruma prawn, *Penaeus japonicus*.";
 RL Aquaticulture 135:205-212(1995).
 CC -1- FUNCTION: ABUNDANT HORMONE FOUND IN THE SINUS GLAND OF ISOPODS AND
 CC DECAPODS WHICH CONTROLS THE BLOOD SUGAR LEVEL. HAS A SECRETAGOGUE
 CC ACTION OVER THE AMYLASE RELEASED FROM THE MIDGUT GLAND. MAY ACT AS
 CC A STRESS HORMONE AND MAY BE INVOLVED IN THE CONTROL OF MOLTING AND
 CC REPRODUCTION.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN
 CC THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE THEY ARE
 CC STORED AND RELEASED.
 CC -1- SIMILARITY: BELONGS TO THE ARTHROPOD CHH/MIH/GIH/YIH FAMILY OF
 CC HORMONES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB007507; BAA22560.1; -;
 DR InterPro: IPR001166; CHH_MIH_GIH.
 DR Pfam: PF01147; Crust_neurohorm; 1.
 DR PRINTS: PR00550; HYPERGLYCEMIC.
 DR PROSITE: PS01250; CHH_MIH_GIH; 1.
 KW Neuropeptide; Hormone; Glucose metabolism; Amidation; Signal;
 KW cleavage on pair of basic residues; Multigene family.
 FT SIGNAL 1 24 POTENTIAL.
 FT PEPTIDE 25 44 CHH PRECURSOR RELATED PEPTIDE (CPRP).
 FT PEPTIDE 47 118 CRUSTACEAN HYPERGLYCEMIC HORMONE 1.
 FT DISULFID 53 89 BY SIMILARITY.
 FT DISULFID 69 85 BY SIMILARITY.
 FT DISULFID 72 98 BY SIMILARITY.
 FT MOD_RES 118 118 AMIDATION (G-119 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 120 AA; 13298 MW; CEC6BE04483897ED CRC64;
 Query Match 25.4%; Score 52.5; DB 1; Length 120;
 Best Local Similarity 41.4%; Pred. No. 7.1;
 Matches 12; Conservative 6; Mismatches 8; Indels 3; Gaps 1;
 QY 10 MIVLVSVILGV---ASHIDNYQPEQS 35
 DB 8 WSAVLASLILLALLAPASPYDAPSPPEAS 36
 RESULT 8
 CHH2_PENUP STANDARD; PRT; 120 AA.
 AC 09U5D2; P81681;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Crustacean hyperglycemic hormone 2 precursor (CHH) (Pej-SGP-II).
 OS Penaeus japonicus (Kuruma prawn).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata;
 OC Penaeoidea; Penaeidae; Marsupenaeus.
 OX NCBI_Taxid=27405;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Eyestalk;
 RA Ohira T., Watanabe T., Aida K., Nagasawa H.;
 RT "Crustacean hyperglycemic hormone of kuruma prawn *Penaeus japonicus*.";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBD databases.
 RP [2]
 RP SEQUENCE OF 47-118.
 RC TISSUE-Sinus gland;

RA MEDLINE-97353924; PubMed-9210164;
RA Yang W.-J., Aida K., Nagasawa H.;
RT "Amino acid sequences and activities of multiple hyperglycemic
RT hormones from the kuruma prawn, Penaeus japonicus.";
RL Peptides 18:479-485(1997).
CC
CC -1- FUNCTION: ABUNDANT HORMONE FOUND IN THE SINUS GLAND OF ISOPODS AND
CC DECAPDS WHICH CONTROLS THE BLOOD SUGAR LEVEL. HAS A SECRETAGOGUE
CC ACTION OVER THE AMYLASE RELEASED FROM THE MIDGUT GLAND. MAY ACT AS
CC A STRESS HORMONE AND MAY BE INVOLVED IN THE CONTROL OF MOLTING AND
CC REPRODUCTION.
CC
CC -1- SIMILARITY: BELONGS TO THE ARTHROPOD CHH/MIH/GIH/VIH FAMILY OF
CC HORMONES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB035724; BAA88339.1; -
CC InterPro: IPR001166; CHH_MIH_GIH.
CC Pfam: PF01147; Crust_neurohorm. 1.
CC PRINTS: PR00550; HYPERGLYCEMIC. 1.
CC PROSITE: PS01250; CHH_MIH_GIH. 1.
CC Neuropeptide; Hormone; Glucose metabolism; Amidation; Signal;
CC Cleavage on pair of basic residues; Multigene family.
CC SIGNAL 1 27
CC PEPTIDE 28 44 CHH PRECURSOR RELATED PEPTIDE (CPRP).
CC PERITIDE 47 118 CRUSTACEAN HYPERGLYCEMIC HORMONE 2.
CC DISULFID 53 89 BY SIMILARITY.
CC FT DISULFID 69 85 BY SIMILARITY.
CC FT DISULFID 72 98 BY SIMILARITY.
CC MOD.RES 118 118 AMIDATION (G-119 PROVIDE AMIDE GROUP).
CC FT MOD.RES 118 118
CC SO SEQUENCE 120 AA; 13467 MW; C2D96499D1231585 CRC64;

Query Match 25.4%; Score 52.5; DB 1; Length 120;
Best Local Similarity 41.4%; Pred. No. 7.1;
Matches 12; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

QY 10 WTIVVSVLLGV---ASHIDNYKPEQS 35
DB 8 WSAALLSLILLALLAPSVDAPSPPEAS 36
ID HEMA_P13HV STANDARD; PRT; 572 AA.
AC P12564;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Human parainfluenza 3 virus (strain Tex/12677/83).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11221;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88101361; PubMed-2827373;
RX van Wyke Coelingh K.L., Winter C.C., Murphy B.R.;
RT "Nucleotide and deduced amino acid sequence of hemagglutinin-
RT neuraminidase genes of human type 3 parainfluenza viruses isolated
RT from 1957 to 1983.";
RL Virology 162:137-143(1988).
CC
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC GLYCOPROTEINS.
CC
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M18764; AAA46851.1; -
CC PIR: P29970; HNNZ83.
CC InterPro: IPR000663; Hem-neuramidse.
CC Pfam: PF00423; HN; 1.
CC KM Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;
CC Transmembrane.
CC FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 32 53
CC FT DOMAIN 54 572
CC FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 572 AA; 64330 MW; 57875F74AC568BED CRC64;

Query Match 25.4%; Score 52.5; DB 1; Length 572;
Best Local Similarity 31.7%; Pred. No. 33;
Matches 13; Conservative 6; Mismatches 11; Indels 11; Gaps 1;

QY 2 NRIELTGMIVLV-----VSILLGVASHIDNYK 31
DB 71 NEFMEITKIQWASDNTNDLIQSGVNTRLTITQSHVNYIP 111
ID DHS_C_RICCN STANDARD; PRT; 124 AA.
AC Q92099;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Succinate dehydrogenase cytochrome b-556 subunit.
GN SDHC OR RC0168.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Malish 7;
RX MEDLINE-21442074; PubMed-11557893;
RX Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RX Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC
CC -1- FUNCTION: MONO-HEME CYTOCHROME OF THE SUCCINATE DEHYDROGENASE
CC COMPLEX.
CC
CC PATHWAY: Lipoic acid cycle.
CC
CC -1- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING FOUR SUBUNITS: A
CC FLAVOPROTEIN, AN IRON-SULFUR, CYTOCHROME B-556, AND AN HYDROPHOBIC
CC ANCHOR PROTEIN.
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B560 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```
DR PROSITE: PS00439; ACYLTRANSF_C_1: 1.
DR PROSITE: PS00440; ACYLTRANSF_C_2: 1.
```

FT	CHAIN	24	307	UBIQUINOL OXIDASE POLYPEPTIDE II.
FT	LIPID	24	24	N-ACYL DIGLYCERIDE (POTENTIAL).
FT	TRANSMEM	46	66	POTENTIAL.
FT		57	107	POTENTIAL.

Query Match 24.9%; Score 51.5; DB 1; Length 307;
 Best Local Similarity 32.5%; Pred. No. 24;
 Matches 13; Conservative 8; Mismatches 14; Indels 5; Gaps 1;

OY 5 IELTGMVIVSVILGAVASHIDNYOPPEOSASVQ 39
 DB 87 IELTGMVIVSVILGAVASHIDNYOPPEOSASVQ 126

RESULT 13

TCR_STRAG STANDARD; PRT; 458 AA.
 ID TCR_STRAG STANDARD; PRT; 458 AA.
 AC P13924;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Tetracycline resistance protein.
 GN TET.

OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus

OX NCBI_TaxID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-90016790; PubMed-2677995;
 RA van der Lelie D., Bron S., Venema G., Oskam L.;

RT "Similarity of minus origins of replication and flanking open reading
 frames of plasmids PUB10, pTR913 and pMW158.";
 RL Nucleic Acids Res. 17:7283-7294(1989).

CC -1 FUNCTION: RESISTANCE TO TETRACYCLINE BY AN ACTIVE TETRACYCLINE
 EFFLUX. THIS IS AN ENERGY-DEPENDENT PROCESS THAT DECREASES THE
 ACCUMULATION OF THE ANTIBIOTIC IN WHOLE CELLS. THIS PROTEIN
 FUNCTIONS AS A METAL-TETRACYCLINE/H+ ANTI-PORTER.

CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1 SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
 AS THE DRUG RESISTANCE TRANSLUCASE FAMILY).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: X15669; CAA33712.1; -

DR PIR: C25599; YTSOG.

DR InterPro: IPR001411; TCR_TetB.

DR PRINTS: PR01036; TCR_TetB.

KW Antibiotic resistance; Transmembrane; Transport; Symport; Plasmid.

FT TRANSMEM 12 33 POTENTIAL.

FT TRANSMEM 81 100 POTENTIAL.

FT TRANSMEM 111 129 POTENTIAL.

FT TRANSMEM 140 162 POTENTIAL.

FT TRANSMEM 165 185 POTENTIAL.

FT TRANSMEM 201 221 POTENTIAL.

FT TRANSMEM 223 240 POTENTIAL.

FT TRANSMEM 256 276 POTENTIAL.

FT TRANSMEM 297 317 POTENTIAL.

FT TRANSMEM 324 344 POTENTIAL.

FT TRANSMEM 346 365 POTENTIAL.

FT TRANSMEM 432 451 POTENTIAL.

FT TRANSMEM 458 477 POTENTIAL.

SEQUENCE 458 AA; 50006 MW; ADZ0147C4199935 CRC64;

Query Match 24.6%; Score 51; DB 1; Length 458;
 Best Local Similarity 28.9%; Pred. No. 41;
 Matches 11; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 4 IELTGMVIVSVILGAVASHIDNYOPPEOSASVQ 41
 DB 343 IELTGMVIVSVILGAVASHIDNYOPPEOSASVQ 380

RESULT 14
 ID YHV2_LACHE STANDARD; PRT; 104 AA.

AC P22295;
 DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 11.8 kDa protein in HTV 5' region precursor (ORF2).

OS Lactobacillus helveticus.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

CC Lactobacillus.

CC NCBI_TaxID=1587;

OX NCBI_TaxID=1587;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-91035244; PubMed-2228964;

RA Joerges M.C., Kleenhammer T.R.;

RT "Cloning, expression, and nucleotide sequence of the Lactobacillus
 helveticus 481 gene encoding the bacteriocin helveticin J.";

RL J. Bacteriol. 172:6339-6347(1990).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: M59360; AAA63273.1; -

DR PIR: B37145; B37145.

KW Hypothetical protein; Signal.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 104 HYPOTHETICAL 11.8 KDA PROTEIN.

SO SEQUENCE 104 AA; 11809 MW; 399818546204C9B CRC64;

Query Match 24.4%; Score 50.5; DB 1; Length 104;
 Best Local Similarity 47.8%; Pred. No. 11;
 Matches 11; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

OY 4 IELTGMVIVSVILGAVASHI 26
 DB 9 IIALAFWIVSVV---GLISHV 28

RESULT 15

CCME_HAEIN

ID CCME_HAEIN STANDARD; PRT; 173 AA.

AC P45036;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cytochrome c-type biogenesis protein ccme.

GN CCME OR H11093.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

CC Haemophilus.

CC NCBI_TaxID=727;

OX NCBI_TaxID=727;

RN [1]
 RP SEQUENCE FROM N.A.

RX STRAIN-Rd / KW20 / ATCC 51907;

RA Fritschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavang A.R., Bull C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goeyne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glöck A., Kelley J.M.,

RA Wiedeman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Ullrich T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Five L.D., Fitchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae

```

RT Rd "
RL Science 269:496-512(1995).
CC -1- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
CC POSSIBLE SUBUNIT OF A HEME LYASE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MOSTLY PERIPLASMIC; ANCHORED IN THE INNER
CC MEMBRANE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE CME/CYCJ FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U32789; AAC22750.1; -.
DR TIGR: H11093; -.
DR InterPro: IPR004329; CME.
DR Pfam: PF03100; CME; 1.
KW Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 30 173 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 173 AA; 19149 MW; 0505AC6B9709156 CRC64;

Query Match 24.4%; Score 50.5; DB 1; Length 173;
Best Local Similarity 40.5%; Pred. No. 18;
Matches 15; Conservative 4; Mismatches 13; Indels 5; Gaps 2;

QY 7 LTGMIVLVSVIILGVASHDNYQPPQASVQ--HK 41
II II : : I I I I I I I I I I
Db 116 LTQPTVLTATFVL--AKHDENVYPPPELGKMKQVHK 149

```

Search completed: February 6, 2003, 21:38:32
 Job time : 13 secs

[illegible]

```
DB 265 RLLILGLMLMLGVLLVTSRLRLHLP 293

RESULT 6
ID 052721 PRELIMINARY; PRT; 440 AA.
AC 052721;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sensor kinase.
GN REGB.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=95095926; PubMed=8002581;
RA Mosley C.S., Suzuki J.Y., Bauer C.E.;
RT "Identification and molecular genetic characterization of a sensor
RT kinase responsible for coordinately regulating light harvesting and
RT reaction center gene expression in response to anaerobiosis [published
RT erratum appears in J Bacteriol 1995 Jun;177(11):3359].";
RL J. Bacteriol. 176:7566-7573(1994).
CC -1 SIMILARITY: TO OTHER PROKARYOTIC SENSOR TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL: L35179; AAA80144.1; -.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003661; His_KinA.
DR InterPro: IPR004359; His_Kin_sig.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; signal; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HisKA; 1.
DR KINASE: Phosphorylation; Sensory transduction; Transferase.
KW KINASE; Phosphorylation; Sensory transduction; Transferase.
SQ SEQUENCE 440 AA; 47410 MW; 8BE58AA65C318C77 CRC64;

Query Match 27.5%; Score 57; DB 2; Length 440;
Best Local Similarity 40.9%; Pred. No. 18;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LIELGTWLVVSVYLLGVASH 25
DB 146 MIEFGSWAIVGVIFLGAVAH 167

RESULT 7
ID 09L906 PRELIMINARY; PRT; 460 AA.
AC 09L906;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sensor kinase.
GN REGB.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=20100775; PubMed=10633119;
RA Chen W., Jager A., Klug G.;
RT "Correction of the DNA sequence of the regB gene of Rhodobacter
RT capsulatus with implications for the membrane topology of the sensor
RT kinase RegB.";
RL J. Bacteriol. 182:818-820(2000).
CC -1 SIMILARITY: TO OTHER PROKARYOTIC SENSOR TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL: AF189160; AA01775.3; -.

DB InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_c.
DR InterPro: IPR003661; His_KinA.
DR InterPro: IPR004359; His_Kin_sig.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; signal; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HisKA; 1.
DR KINASE: Phosphorylation; Sensory transduction; Transferase.
KW KINASE; Phosphorylation; Sensory transduction; Transferase.
SQ SEQUENCE 460 AA; 50101 MW; BFB06EFB75C3A1E4 CRC64;

Query Match 27.5%; Score 57; DB 2; Length 460;
Best Local Similarity 40.9%; Pred. No. 19;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LIELGTWLVVSVYLLGVASH 25
DB 166 MIEFGSWAIVGVIFLGAVAH 187

RESULT 8
ID 09UVB5 PRELIMINARY; PRT; 826 AA.
AC 09UVB5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein mannosyltransferase.
GN PMT6.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1006;
RX MEDLINE=20270133; PubMed=10809683;
RA Timpel C., Zink S., Strahl-Bolsinger S., Schroppel K., Ernst J.;
RT "Morphogenesis, adhesive properties, and antifungal resistance depend
RT on the pmt6 protein mannosyltransferase in the fungal pathogen Candida
RT albicans.";
RL J. Bacteriol. 182:3063-3071(2000).
DR EMBL: AF104916; AAFL6867.1; -.
DR InterPro: IPR003608; MIR.
DR InterPro: IPR00342; PMT.
DR Pfam: PF02815; MIR; 3.
DR Pfam: PF02366; PMT; 1.
DR SMART: SM00472; MIR; 3.
DR GLYCOSYLTRANSFERASE: Transferase.
KW GLYCOSYLTRANSFERASE; Transferase.
SQ SEQUENCE 826 AA; 94294 MW; B3DE7538C1F8FB7 CRC64;

Query Match 27.5%; Score 57; DB 3; Length 826;
Best Local Similarity 35.7%; Pred. No. 36;
Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 4 LIELGTWLVVSVYLLGVASHINDYOP 31
DB 729 LLPLAGWVLAHYVPLIMGRVKKYLLHHYVP 756

RESULT 9
ID 08UW68 PRELIMINARY; PRT; 309 AA.
AC 08UW68;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AF290615-like protein.
GN AF290615-LIKE.
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
```

OC	Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC	Tetraodontidae; Tetraodon.
OX	NCBI_TaxID=99883;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bernot A.
RT	*Analysis of 148 kb of genomic DNA of Tetraodon nigroviridis covering
RL	an amylase gene family.
DR	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
SQ	EMBL: AJ308233; CAC87122.1; -
QY	SEQUENCE 309 AA; 35327 MW; AF93C122AF1FE094 CRC64;
Query Match	
Best Local Similarity	27.3%; Score 56.5; DB 13; Length 309;
Matches	15; Conservative 7; Mismatches 6; Indels 9; Gaps 2;
Db	7 LTGMIV---LVSVYLL-----GVASHIDNYQPPDQ 34
	: :
	231 LFGMILTTTLVSLVLIWICCATVATVADQYTPAEK 267
RESULT 10	
ID	Q8QFS3 PRELIMINARY; PRT; 318 AA.
AC	Q8QFS3;
DT	01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-JUN-2002 (TREMBLrel. 21, last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE	H01CJC protein.
OS	H01CJC.
OC	Tetraodon nigroviridis (Green puffer).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC	Tetraodontidae; Tetraodon.
OX	NCBI_TaxID=99883;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bernot A.
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Bouneau L.
RT	*Analysis of 148 kb of genomic DNA of Tetraodon nigroviridis covering
RL	an amylase gene family.
DR	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
SQ	EMBL: AJ427223; CAD20261.1; -
QY	SEQUENCE 318 AA; 36409 MW; 42F2952DC770005A CRC64;
Query Match	
Best Local Similarity	27.3%; Score 56.5; DB 13; Length 318;
Matches	15; Conservative 7; Mismatches 6; Indels 9; Gaps 2;
Db	7 LTGMIV---LVSVYLL-----GVASHIDNYQPPDQ 34
	: :
	240 LFGMILTTTLVSLVLIWICCATVATVADQYTPAEK 276
RESULT 11	
ID	Q9XBMI PRELIMINARY; PRT; 490 AA.
AC	Q9XBMI;
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE	Alkane 1-monooxygenase (EC 1.14.15.3).
GN	ALKB.
OS	Prauserella rugosa.
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC	Actinomycetales; Pseudonocardiales; Pseudonocardaceae; Prauserella.
OX	NCBI_TaxID=43354;
RN	[1]
RP	SEQUENCE FROM N.A.

RC	STRAIN-NRRL B-2295;
RX	MEDLINE-21128526; PubMed=11207749;
RA	Smits T.H.M., Roeluisberger M., Wittholt B., Van Bellen J.B.;
RT	*Molecular screening for alkane hydroxylase genes in Gram-negative and
RT	Gram-positive bacteria."
RL	Environ. Microbiol. 1:307-317(1999)
DR	EMBL: AJ009587; CAB51024.2; -
DR	HSSP: P00268; 5RXN.
DR	InterPro: IPR001225; FA_desaturase.
DR	InterPro: IPR004039; Rubredox.
DR	InterPro: IPR001052; Rubredoxin.
DR	Pfam: PF00487; FA_desaturase; 1.
DR	Pfam: PF00301; rubredoxin; 1.
DR	PRINTS: PR00163; RUBREDOXIN.
DR	ProDom: PD001610; Rubredoxin; 1.
DR	PROSITE: PS00202; RUBREDOXIN; 1.
KW	Monooxygenase; Oxidoreductase.
SQ	SEQUENCE 490 AA; 54700 MW; 83FAEA25D05B5848 CRC64;
Query Match	
Best Local Similarity	27.1%; Score 56; DB 2; Length 490;
Matches	14; Conservative 6; Mismatches 10; Indels 8; Gaps 1;
QY	4 LIELTGM-----IVLVSVILGVASHIDNYQPPDQ 33
	: :
Db	50 LREATGMGLWMTGPIVILVVPDLVLVAGLDRSNPD 87
RESULT 12	
ID	Q8XN66 PRELIMINARY; PRT; 623 AA.
AC	Q8XN66;
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE	Probable ABC transporter.
OS	CPE0472.
OC	Clostridium perfringens.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC	Clostridiales; Clostridiaceae; Clostridium.
OX	NCBI_TaxID=1502;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-13 / TYPE A;
RX	PubMed=11792842;
RA	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.;
RA	Shida T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT	*Complete genome sequence of Clostridium perfringens, an anaerobic
RT	flesh-eater."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR	EMBL: AP003186; BAB80178.1; -
DR	InterPro: IPR003593; AAA_ATPase.
DR	InterPro: IPR001140; ABCtransporter.
DR	InterPro: IPR003439; ABC_transporter.
DR	Pfam: PF00664; ABC_membrane; 1.
DR	Pfam: PF00005; ABC_tran; 1.
DR	ProDom: PD000006; ABC_transporter; 1.
DR	SMART: SM00382; AAA; 1.
DR	PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW	Complete proteome.
SQ	SEQUENCE 623 AA; 69773 MW; AFD599795F257FA9 CRC64;
Query Match	
Best Local Similarity	26.8%; Score 55.5; DB 16; Length 623;
Matches	11; Conservative 11; Mismatches 10; Indels 5; Gaps 1;
QY	10 WIVLVSVILGVASH-----IDNYQPPDQASVQHK 41
	: :
Db	64 WLVIVASIMLNIITSYPIISLINTYTSKMSQTLQK 100
RESULT 13	
Q97P36	

	Query Match	26.6%	Score 55;	DB 16;	Length 219;
	Best Local Similarity	40.9%	Pred. No. 16;		
	Matches 9;	Conservative	8;	Mismatches 5;	Indels 0;
QY	4	LIEETGWTIVLVSVLLIGVASH	25		
		: : : : : :			
Db	127	LIASSGWNVLVMSFLIDILGH	148		

RESULT 14			
ID	Q9CEA7	PRELIMINARY;	PRT; 320 AA.
AC	Q9CEA7;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Hypothetical protein yqbf.		
GN	YQBF OR L11574.		
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;		
CC	Streptococcaceae; Lactococcus.		
OX	NCBI_TaxID=1360;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-IL1403;		
RX	MEDLINE=21235186; PubMed=1137471;		
RA	Boletín A., Wincker P., Manger S., Jaillon O., Malarre K.,		
RA	Weissenbach J., Ehrlich S.D., Sorkin A.;		
RT	"The complete genome sequence of the lactic acid bacterium Lactococcus		
RT	lactis ssp. lactis IL1403."		
RL	Genome RES. 11:731-757(2001).		
DR	EMBL: AE006388; AAK05672.1;		
DR	InterPro: IPR003083; AB_Hydrolase.		
DR	InterPro: IPR000379; Lipase.		
DR	InterPro: IPR000379; Ser-estrs._site.		
DR	PRINTS: PR00111; ABHYDROLASE.		
DR	PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.		
KW	Hypothetical protein; Complete proteome.		
QC	SEQUENCE 320 AA; 35901 MW; 2E706FBD803461A CRC64;		

RESULT 15	
Q93JR2	
ID Q93JR2	PRELIMINARY;
100770	PRT; 183 AA

AC Q93J0R2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Alkane-1-monooxygenase (Fragment).
 GN ALKB.
 OS Rhodococcus fascians.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus
 OX NCBI_TaxID=1828;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=154-S;
 RA Van Bellen J.B., Smits T.H.M., Balada S.B., Witholt B.;
 RT "Alkane hydroxylases in Gram-positive strains."
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL, AJ301873; CAC040950.1. --
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR PRINTS: PRO1565; NEUROMEDINUR.
 KW Monoxygenase.
 FT NON_TER 1 1
 FT NON_TER 183 183
 SQ SEQUENCE 183 AA; 21185 MW; 7576490877866D0 CRC64;

	Query Match	26.3%	Score 54.5	DB 2	Length 183
	Best Local Similarity	25.5%	Pred. No. 15		
	Matches 13	Conservative 13	Mismatches 12	Indels 13	Gaps 2
QY	4 LIEITGWIVL-----VVSYLLGLGVASHINDRY-----QPEQSASVYOK 41				
	:				
	:				
	:				
	:				
Db	106 LIAVFGWIVLPEYLLLOAIAIVLYEAAVLEHYGMRTRRRDPGRRAKSSHR 156				

```
Search completed: February 6, 2003, 21:39:09
Job time : 33 secs
```